

AMENDMENTS TO THE CLAIMS

1-50. (Canceled)

51. (Previously presented) A method for identifying a subspecies of *Staphylococcus aureus*, the method comprising:

obtaining a sample of a microorganism;

sequencing a first region of a nucleic acid from the microorganism sample;

comparing the first sequenced region with historical sequence data stored in a database, the historical sequence data comprising at least one *Staphylococcus aureus* sequence region; and

determining a measure of phylogenetic relatedness between the microorganism sample and a plurality of historical samples stored in the database,

wherein the at least one *Staphylococcus aureus* sequence region further comprises a forward primer upstream of the sequence and a reverse primer downstream of the sequence, and the forward primer and the reverse primer permit identification of a region of variable number tandem repeats.

52. (Previously presented) The method of claim 51, wherein the at least one *Staphylococcus aureus* sequence region has a mutation rate sufficient to differentiate between subspecies of *Staphylococcus aureus* to determine phylogenetic relatedness and to track the microorganism.

53. (Previously presented) The method of claim 51, wherein the *Staphylococcus aureus* sequence regions comprise a region of variable number tandem repeats.

54. (Previously presented) The method of claim 53, wherein the region of variable number of tandem repeats comprise at least one sequence selected from the group consisting of SEQ ID NO 55, SEQ ID NO 57, SEQ ID NO 58, SEQ ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64, SEQ ID NO 65, SEQ ID NO 66,

SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, SEQ ID NO 74, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO 80.

55. (Previously presented) The method of claim 54, wherein the region of variable number of tandem repeats further comprise at least one point mutation in at least one sequence.

56. (Previously presented) The method of claim 55, wherein the number of point mutations is sufficient to identify the sequence and determine the phylogenetic relatedness of microorganisms including the sequence in their genome.

57. (Previously presented) The method of claim 55, wherein the at least one point mutation is not in the first three nucleotides of the at least one sequence.

58. (Previously presented) The method of claim 51, wherein the forward primer comprises SEQ ID NO 75 and the reverse primer comprises SEQ ID NO 76.

59. (Previously presented) The method of claim 58, wherein the forward primer comprises SEQ ID NO 76 and the reverse primer comprises SEQ ID NO 77.

60. (Previously presented) The method of claim 54, wherein the first three nucleotides of the at least one sequence are GAT or GAC.

61. (Previously presented) The method of claim 54, wherein the region of variable number of tandem repeats comprises more than one copy of at least one sequence selected from the group consisting of SEQ ID NO 55, SEQ ID NO 57, SEQ ID NO 58, SEQ ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64, SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, SEQ ID NO 74, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO 80.

62. (Previously presented) The method of claim 51, wherein the historical sequence data comprises the sequence of SEQ ID NO 54.

63. (Previously presented) The method of claim 53, wherein the region of variable number of tandem repeats is sufficient to determine the phylogenetic relatedness between the microorganism sample and the plurality of historical samples stored in the database.

64-87. (Canceled).